

RAW SEQUENCE LISTING

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Application Serial Number: 10|511,756
Source: TFWQ
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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/511,756

DATE: 02/08/2006
 TIME: 11:42:31

Input Set : A:\12177804.APP
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3 <110> APPLICANT: BERGMANN, ANDREAS
 4 STRUCK, JOACHIM
 5 UHLEIN, MONIKA
 7 <120> TITLE OF INVENTION: USES OF CARBAMOYL PHOSPHATE SYNTHETASE 1 (CPS 1) AND
 8 ITS FRAGMENTS FOR THE DIAGNOSIS OF INFLAMMATORY
 9 DISEASES AND SEPSIS
 11 <130> FILE REFERENCE: 121778-04341933
 13 <140> CURRENT APPLICATION NUMBER: 10/511,756
 C--> 14 <141> CURRENT FILING DATE: 2004-10-19
 16 <150> PRIOR APPLICATION NUMBER: PCT/EP03/03939
 17 <151> PRIOR FILING DATE: 2003-04-15
 19 <150> PRIOR APPLICATION NUMBER: EP 020088415
 20 <151> PRIOR FILING DATE: 2002-04-19
 22 <160> NUMBER OF SEQ ID NOS: 8
 24 <170> SOFTWARE: PatentIn Ver. 2.1
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 11
 28 <212> TYPE: PRT
 29 <213> ORGANISM: Homo sapiens
 31 <400> SEQUENCE: 1
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 37 <210> SEQ ID NO: 2
 38 <211> LENGTH: 7
 39 <212> TYPE: PRT
 40 <213> ORGANISM: Homo sapiens
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 43 Asn Gln Pro Val Leu Asn Ile
 44 1 5
 48 <210> SEQ ID NO: 3
 49 <211> LENGTH: 13
 50 <212> TYPE: PRT
 51 <213> ORGANISM: Homo sapiens
 53 <400> SEQUENCE: 3
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 55 1 5 10
 59 <210> SEQ ID NO: 4
 60 <211> LENGTH: 4
 61 <212> TYPE: PRT
 62 <213> ORGANISM: Homo sapiens
 64 <400> SEQUENCE: 4
 65 Thr Ala His Ile
 66 1

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70 <210> SEQ ID NO: 5
71 <211> LENGTH: 12
72 <212> TYPE: PRT
73 <213> ORGANISM: Homo sapiens
75 <400> SEQUENCE: 5
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82 <211> LENGTH: 1500
83 <212> TYPE: PRT
84 <213> ORGANISM: Homo sapiens
86 <400> SEQUENCE: 6
87 Met Thr Arg Ile Leu Thr Ala Phe Lys Val Val Arg Thr Leu Lys Thr
88 1 5 10 15
90 Gly Phe Gly Phe Thr Asn Val Thr Ala His Gln Lys Trp Lys Phe Ser
91 20 25 30
93 Arg Pro Gly Ile Arg Leu Leu Ser Val Lys Ala Gln Thr Ala His Ile
94 35 40 45
96 Val Leu Glu Asp Gly Thr Lys Met Lys Gly Tyr Ser Phe Gly His Pro
97 50 55 60
99 Ser Ser Val Ala Gly Glu Val Val Phe Asn Thr Gly Leu Gly Gly Tyr
100 65 70 75 80
102 Pro Glu Ala Ile Thr Asp Pro Ala Tyr Lys Gly Gln Ile Leu Thr Met
103 85 90 95
105 Ala Asn Pro Ile Ile Gly Asn Gly Gly Ala Pro Asp Thr Thr Ala Leu
106 100 105 110
108 Asp Glu Leu Gly Leu Ser Lys Tyr Leu Glu Ser Asn Gly Ile Lys Val
109 115 120 125
111 Ser Gly Leu Leu Val Leu Asp Tyr Ser Lys Asp Tyr Asn His Trp Leu
112 130 135 140
114 Ala Thr Lys Ser Leu Gly Gln Trp Leu Gln Glu Lys Val Pro Ala
115 145 150 155 160
117 Ile Tyr Gly Val Asp Thr Arg Met Leu Thr Lys Ile Ile Arg Asp Lys
118 165 170 175
120 Gly Thr Met Leu Gly Lys Ile Glu Phe Glu Gly Gln Pro Val Asp Phe
121 180 185 190
123 Val Asp Pro Asn Lys Gln Asn Leu Ile Ala Glu Val Ser Thr Lys Asp
124 195 200 205
126 Val Lys Val Tyr Gly Lys Gly Asn Pro Thr Lys Val Val Ala Val Asp
127 210 215 220
129 Cys Gly Ile Lys Asn Asn Val Ile Arg Leu Leu Val Lys Arg Gly Ala
130 225 230 235 240
132 Glu Val His Leu Val Pro Trp Asn His Asp Phe Thr Lys Met Glu Tyr
133 245 250 255
135 Asp Gly Ile Leu Ile Ala Gly Gly Pro Gly Asn Pro Ala Leu Ala Glu
136 260 265 270
138 Pro Leu Ile Gln Asn Val Arg Lys Ile Leu Glu Ser Asp Arg Lys Glu
139 275 280 285
141 Pro Leu Phe Gly Ile Ser Thr Gly Asn Leu Ile Thr Gly Leu Ala Ala

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142	290	295	300
144	Gly Ala Lys Thr Tyr Lys	Met Ser Met Ala Asn Arg	Gly Gln Asn Gln
145	305	310	315
147	320	325	330
148	335	340	345
150	350	355	360
151	365	370	375
153	380	385	390
154	395	400	405
156	415	420	425
157	430	435	440
159	445	450	455
160	460	465	470
162	475	480	485
163	495	500	505
165	510	515	520
166	525	530	535
168	540	545	550
169	555	560	565
171	570	575	580
172	590	595	600
174	595	605	610
175	620	625	630
177	640	645	650
178	655	660	665
180	670	675	680
181	685		

142 290 295 300
144 Gly Ala Lys Thr Tyr Lys Met Ser Met Ala Asn Arg Gly Gln Asn Gln
145 305 310 315 320
147 Pro Val Leu Asn Ile Thr Asn Lys Gln Ala Phe Ile Thr Ala Gln Asn
148 325 330 335
150 His Gly Tyr Ala Leu Asp Asn Thr Leu Pro Ala Gly Trp Lys Pro Leu
151 340 345 350
153 Phe Val Asn Val Asn Asp Gln Thr Asn Glu Gly Ile Met His Glu Ser
154 355 360 365
156 Lys Pro Phe Phe Ala Val Gln Phe His Pro Glu Val Thr Pro Gly Pro
157 370 375 380
159 Ile Asp Thr Glu Tyr Leu Phe Asp Ser Phe Phe Ser Leu Ile Lys Lys
160 385 390 395 400
162 Gly Lys Ala Thr Thr Ile Thr Ser Val Leu Pro Lys Pro Ala Leu Val
163 405 410 415
165 Ala Ser Arg Val Glu Val Ser Lys Val Leu Ile Leu Gly Ser Gly Gly
166 420 425 430
168 Leu Ser Ile Gly Gln Ala Gly Glu Phe Asp Tyr Ser Gly Ser Gln Ala
169 435 440 445
171 Val Lys Ala Met Lys Glu Glu Asn Val Lys Thr Val Leu Met Asn Pro
172 450 455 460
174 Asn Ile Ala Ser Val Gln Thr Asn Glu Val Gly Leu Lys Gln Ala Asp
175 465 470 475 480
177 Thr Val Tyr Phe Leu Pro Ile Thr Pro Gln Phe Val Thr Glu Val Ile
178 485 490 495
180 Lys Ala Glu Gln Pro Asp Gly Leu Ile Leu Gly Met Gly Gly Gln Thr
181 500 505 510
183 Ala Leu Asn Cys Gly Val Glu Leu Phe Lys Arg Gly Val Leu Lys Glu
184 515 520 525
186 Tyr Gly Val Lys Val Leu Gly Thr Ser Val Glu Ser Ile Met Ala Thr
187 530 535 540
189 Glu Asp Arg Gln Leu Phe Ser Asp Lys Leu Asn Glu Ile Asn Glu Lys
190 545 550 555 560
192 Ile Ala Pro Ser Phe Ala Val Glu Ser Ile Glu Asp Ala Leu Lys Ala
193 565 570 575
195 Ala Asp Thr Ile Gly Tyr Pro Val Met Ile Arg Ser Ala Tyr Ala Leu
196 580 585 590
198 Gly Gly Leu Gly Ser Gly Ile Cys Pro Asn Arg Glu Thr Leu Met Asp
199 595 600 605
201 Leu Ser Thr Lys Ala Phe Ala Met Thr Asn Gln Ile Leu Val Glu Lys
202 610 615 620
204 Ser Val Thr Gly Trp Lys Glu Ile Glu Tyr Glu Val Val Arg Asp Ala
205 625 630 635 640
207 Asp Asp Asn Cys Val Thr Val Cys Asn Met Glu Asn Val Asp Ala Met
208 645 650 655
210 Gly Val His Thr Gly Asp Ser Val Val Val Ala Pro Ala Gln Thr Leu
211 660 665 670
213 Ser Asn Ala Glu Phe Gln Met Leu Arg Arg Thr Ser Ile Asn Val Val
214 675 680 685

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216 Arg His Leu Gly Ile Val Gly Glu Cys Asn Ile Gln Phe Ala Leu His
217 690 695 700
219 Pro Thr Ser Met Glu Tyr Cys Ile Ile Glu Val Asn Ala Arg Leu Ser
220 705 710 715 720
222 Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr Gly Tyr Pro Leu Ala Phe
223 725 730 735
225 Ile Ala Ala Lys Ile Ala Leu Gly Ile Pro Leu Pro Glu Ile Lys Asn
226 740 745 750
228 Val Val Ser Gly Lys Thr Ser Ala Cys Phe Glu Pro Ser Leu Asp Tyr
229 755 760 765
231 Met Val Thr Lys Ile Pro Arg Trp Asp Leu Asp Arg Phe His Gly Thr
232 770 775 780
234 Ser Ser Arg Ile Gly Ser Ser Met Lys Ser Val Gly Glu Val Met Ala
235 785 790 795 800
237 Ile Gly Arg Thr Phe Glu Glu Ser Phe Gln Lys Ala Leu Arg Met Cys
238 805 810 815
240 His Pro Ser Ile Glu Gly Phe Thr Pro Arg Leu Pro Met Asn Lys Glu
241 820 825 830
243 Trp Pro Ser Asn Leu Asp Leu Arg Lys Glu Leu Ser Glu Pro Ser Ser
244 835 840 845
246 Thr Arg Ile Tyr Ala Ile Ala Lys Ala Ile Asp Asp Asn Met Ser Leu
247 850 855 860
249 Asp Glu Ile Glu Lys Leu Thr Tyr Ile Asp Lys Trp Phe Leu Tyr Lys
250 865 870 875 880
252 Met Arg Asp Ile Leu Asn Met Glu Lys Thr Leu Lys Gly Leu Asn Ser
253 885 890 895
255 Glu Ser Met Thr Glu Glu Thr Leu Lys Arg Ala Lys Glu Ile Gly Phe
256 900 905 910
258 Ser Asp Lys Gln Ile Ser Lys Cys Leu Gly Leu Thr Glu Ala Gln Thr
259 915 920 925
261 Arg Glu Leu Arg Leu Lys Lys Asn Ile His Pro Trp Val Lys Gln Ile
262 930 935 940
264 Asp Thr Leu Ala Ala Glu Tyr Pro Ser Val Thr Asn Tyr Leu Tyr Val
265 945 950 955 960
267 Thr Tyr Asn Gly Gln Glu His Asp Val Asn Phe Asp Asp His Gly Met
268 965 970 975
270 Met Val Leu Gly Cys Gly Pro Tyr His Ile Gly Ser Ser Val Glu Phe
271 980 985 990
273 Asp Trp Cys Ala Val Ser Ser Ile Arg Thr Leu Arg Gln Leu Gly Lys
274 995 1000 1005
276 Lys Thr Val Val Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Phe
277 1010 1015 1020
279 Asp Glu Cys Asp Lys Leu Tyr Phe Glu Glu Leu Ser Leu Glu Arg Ile
280 1025 1030 1035 1040
282 Leu Asp Ile Tyr His Gln Glu Ala Cys Gly Gly Cys Ile Ile Ser Val
283 1045 1050 1055
285 Gly Gly Gln Ile Pro Asn Asn Leu Ala Val Pro Leu Tyr Lys Asn Gly
286 1060 1065 1070
288 Val Lys Ile Met Gly Thr Ser Pro Leu Gln Ile Asp Arg Ala Glu Asp

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289	1075	1080	1085	
291	Arg Ser Ile Phe Ser Ala Val Leu Asp Glu Leu Lys Val Ala Gln Ala			
292	1090	1095	1100	
294	Pro Trp Lys Ala Val Asn Thr Leu Asn Glu Ala Leu Glu Phe Ala Lys			
295	1105	1110	1115	1120
297	Ser Val Asp Tyr Pro Cys Leu Leu Arg Pro Ser Tyr Val Leu Ser Gly			
298	1125	1130	1135	
300	Ser Ala Met Asn Val Val Phe Ser Glu Asp Glu Met Lys Lys Phe Leu			
301	1140	1145	1150	
303	Glu Glu Ala Thr Arg Val Ser Gln Glu His Pro Val Val Leu Thr Lys			
304	1155	1160	1165	
306	Phe Val Glu Gly Ala Arg Glu Val Glu Met Asp Ala Val Gly Lys Asp			
307	1170	1175	1180	
309	Gly Arg Val Ile Ser His Ala Ile Ser Glu His Val Glu Asp Ala Gly			
310	1185	1190	1195	1200
312	Val His Ser Gly Asp Ala Thr Leu Met Leu Pro Thr Gln Thr Ile Ser			
313	1205	1210	1215	
315	Gln Gly Ala Ile Glu Lys Val Lys Asp Ala Thr Arg Lys Ile Ala Lys			
316	1220	1225	1230	
318	Ala Phe Ala Ile Ser Gly Pro Phe Asn Val Gln Phe Leu Val Lys Gly			
319	1235	1240	1245	
321	Asn Asp Val Leu Val Ile Glu Cys Asn Leu Arg Ala Ser Arg Ser Phe			
322	1250	1255	1260	
324	Pro Phe Val Ser Lys Thr Leu Gly Val Asp Phe Ile Asp Val Ala Thr			
325	1265	1270	1275	1280
327	Lys Val Met Ile Gly Glu Asn Val Asp Glu Lys His Leu Pro Thr Leu			
328	1285	1290	1295	
330	Asp His Pro Ile Ile Pro Ala Asp Tyr Val Ala Ile Lys Ala Pro Met			
331	1300	1305	1310	
333	Phe Ser Trp Pro Arg Leu Arg Asp Ala Asp Pro Ile Leu Arg Cys Glu			
334	1315	1320	1325	
336	Met Ala Ser Thr Gly Glu Val Ala Cys Phe Gly Glu Gly Ile His Thr			
337	1330	1335	1340	
339	Ala Phe Leu Lys Ala Met Leu Ser Thr Gly Phe Lys Ile Pro Gln Lys			
340	1345	1350	1355	1360
342	Gly Ile Leu Ile Gly Ile Gln Gln Ser Phe Arg Pro Arg Phe Leu Gly			
343	1365	1370	1375	
345	Val Ala Glu Gln Leu His Asn Glu Gly Phe Lys Leu Phe Ala Thr Glu			
346	1380	1385	1390	
348	Ala Thr Ser Asp Trp Leu Asn Ala Asn Asn Val Pro Ala Thr Pro Val			
349	1395	1400	1405	
351	Ala Trp Pro Ser Gln Glu Gly Gln Asn Pro Ser Leu Ser Ser Ile Arg			
352	1410	1415	1420	
354	Lys Leu Ile Arg Asp Gly Ser Ile Asp Leu Val Ile Asn Leu Pro Asn			
355	1425	1430	1435	1440
357	Asn Asn Thr Lys Phe Val His Asp Asn Tyr Val Ile Arg Arg Thr Ala			
358	1445	1450	1455	
360	Val Asp Ser Gly Ile Pro Leu Leu Thr Asn Phe Gln Val Thr Lys Leu			
361	1460	1465	1470	

VERIFICATION SUMMARY

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